Amendments to the Specification

Please replace the paragraph beginning at page 16, line 26, with the following rewritten paragraph:

Fig. 1 A and B show[[s]] the deduced amino acid sequence (SEQ ID NO: 1) of human *mpl* ligand (hML) cDNA and the coding nucleotide sequence (SEQ ID NO: 2). Nucleotides are numbered at the beginning of each line. The 5' and 3' untranslated regions are indicated in lower case letters. Amino acid residues are numbered above the sequence starting at Ser 1 of the mature m*pl* ligand (ML) protein sequence. The boundaries of presumed exon 3 are indicated by the arrows and the potential N-glycosylation sites are boxed. Cysteine residues are indicated by a dot above the sequence. The underlined sequence corresponds to the N-terminal sequence determined from *mpl* ligand purified from porcine plasma.

Please replace the paragraph beginning at page 17, line 1, with the following rewritten paragraph:

Fig. 2 A and B show[[s]] the procedure used for the *mpl* ligand ^{3}H-thymidine incorporation assay. To determine the presence of *mpl* ligand from various sources, the *mpl* P Ba/F3 cells were starved of IL-3 for 24 hours in a humidified incubator at 37°C in 5% CO_2 and air. Following IL-3 starvation the cells were plated out in 96 well culture dishes with or without diluted samples and cultured for 24 hrs in a cell culture incubator. 20 µl of serum free RPMI media containing 1 µCi of ^{3}H-thymidine was added to each well for the last 6-8 hours. The cells were then harvested on 96 well filter plates and washed with water. The filters were then counted.

Please replace the paragraphs beginning at page 18, line 21, with the following rewritten paragraph:

Fig. 11 A and B show[[s]] deduced amino acid sequence of mature human *mpl ligand* isoforms h-ML (SEQ ID NO: 6), h-ML2 (SEQ ID NO: 8), h-ML3 (SEQ ID NO: 9), and h-ML4 (SEQ ID

NO: 10). Identical amino acids are boxed and gaps introduced for optimal alignment are indicated by dashes.

Fig. 12 A-12~~C~~D show[[s]] the effect of human *mpl* ligand on *8a1F3-mpl* cell proliferation (A), in *vitro* human megakaryocytopoiesis quantitated using a radio labeled murine IgG monoclonal antibody specific to the megakaryocyte glycoprotein GPIIbIIIa (B), and murine thrombopoiesis measured 30 in a platelet rebound assay (C and D).

Two hundred ninety-three cells were transfected by the $CaPO_4$ method (Gorman, C in *DNA Cloning:* A *New Approach* 2:143-190 [1985]) with pRK5 vector alone, pRK5-hML or with pRK5-ML_{153} overnight (pRK5-ML_{153} was generated by introducing a stop codon after residue 153 of hML by PCR). Media was then conditioned for 36h and assayed for stimulation of 35 cell proliferation of Ba/F3-*mpl* as described in **Example 1** (A) or in *vitro* human megakaryocytopoiesis (B). Megakaryocytopoiesis was quantitated using a ^{125}1 radiolabeled murine IgG monoclonal antibody (HP1-1D) to the megakaryocyte specific glycoprotein GPIIbIIIa as described (Grant *at al. Blood* 69:1334-1339 [1987]). The effect of partially purified recombinant ML (rML) on *in vivo* platelet production (C and D) was determined using the rebound thrombocytosis assay described by McDonald, T.P. *Proc. Soc. Exp. Biol. Med.* 5 144:1006-10012 (1973). Partially purified rML was prepared from 200ml of conditioned media containing the recombinant ML. The media was passed through a 2ml Blue-Sepharose column equilibrated in PBS and the column was washed with PBS and eluted with PBS containing 2M each of urea and NaCl. The active fraction was dialyzed into PBS and made 1 mg/ml with endotoxin free BSA. The sample contained less than one unit of endotoxin /ml. Mice were injected with either 64,000, 32,000 or 16,000 units of rML or excipient alone. Each group consisted of six mice. The mean and standard deviation of each group is shown. p values were determined by a 2 tailed T -test comparing medians.

Please replace the paragraphs beginning at page 19, line 17, with the following rewritten paragraph:

Fig. 14 A and B show[[s]] the nucleotide sequence: cDNA coding (SEQ ID NO: 11) and deduced amino acid sequence (SEQ ID NO: 12) of the open reading frame of a murine ML isoform. This mature murine *mpl* ligand isoform contains 331 amino acid residues, four fewer than the putative full length mML, and is therefore designated mML2. Nucleotides are numbered at the beginning of each line. Amino acid residues are numbered above the sequence starting with Ser 1. The potential N-glycosylation sites are underlined. Cysteine residues are indicated by a dot above the sequence.

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Fig. 15 A and B show[[s]] the cDNA sequence (SEQ ID NO: 13) and predicted protein sequence (SEQ ID NO: 14) of this murine ML isoform (mML). Nucleotides are numbered at the beginning of each line. Amino acid residues are numbered above the sequence starting with Ser 1. This mature murine *mpl* ligand isoform contains 335 amino acid residues and is believed to be the full length *mpl* ligand. designated mML. The signal sequence is indicated with a dashed underline and the likely cleavage point is denoted with an arrow. The 5' and 3' untranslated regions are indicated with lower case letters. The two deletions found as a result of alternative splicing (mML2 and mML3) are underlined. The four cysteine residues are indicated by a dot. The seven potential N-glycosylation sites are boxed.

Please replace the paragraphs beginning at page 20, line 16, with the following rewritten paragraph:

Fig. 17 A and B compare[[s]] the predicted amino acid sequences of mature ML isoforms from mouse-ML (SEQ ID NO: 16), pig-ML (SEQ ID NO: 17) and human-ML (SEQ ID NO: 6). Amino acid sequences are aligned with gaps, indicated by dashes, introduced for optimal alignment. Amino acids are numbered at the beginning of each line with identical residues boxed. Potential N-glycosylation sites are indicated by a shaded box and cysteine residues are designated with a dot. The conserved di-basic amino acid motif that presents a potential protease cleavage site is underlined. The four amino acid deletion found to occur in all three species (ML2) is outlined with a bold box.

Fig. 18 A and B show[[s]] the cDNA sequence (SEQ ID NO: 18) and predicted mature protein sequence(SEQ ID NO: 17) of a porcine ML isoform (pML). This porcine *mpl* ligand isoform contains 332 amino acid residues and is believed to be the full length porcine *mpl* ligand, designated pML. Nucleotides are numbered at the beginning of each line. Amino acid residues are numbered above the sequence starting with Ser 1.

Fig. 19 A and B show[[s]] the cDNA sequence (SEQ ID NO: 19) and predicted mature protein sequence(SEQ ID NO: 20) of a porcine ML isoform (pML2). This porcine *mpl* ligand isoform contains 328 amino acid residues and is a four residue[[s]] deletion form of the full length porcine *mpl* ligand, designated pML2. Nucleotides are numbered at the beginning of each line. Amino acid residues are numbered above the sequence starting with Ser 1.

Fig. 20 A and B compare[[s]] the deduced amino acid sequence of the full length porcine ML isoform pML(SEQ ID NO: 17) and a porcine ML isoform designated pML2 (SEQ ID NO: 20). The predicted amino acid sequence for the pML is aligned with pML2 sequence. Identical amino acids are boxed and gaps introduced for optimal alignment are indicated by dashes. Amino acids are numbered at the beginning of each line.